RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/660,811*

Source: *1FWO*

Date Processed by STIC: *3/12/04*

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PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

> http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
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Revised 10/08/03

RAW SEQUENCE LISTING   DATE: 03/12/2004
PATENT APPLICATION: **US/10/660,811**   TIME: 09:13:21

    Input Set : **A:\00786.435003.SEQLIST.TXT**
    Output Set: **N:\CRF4\03122004\J660811.raw**

```
 4 <110> APPLICANT: Rahme, Laurence
 5        He, Jianxin
 6        Baldini, Regina
 7        Solsbacher, Jens
 8        Wagner, Peter
10 <120> TITLE OF INVENTION: Virulence-Associated Nucleic Acids and
11        Proteins and Uses Thereof
14 <130> FILE REFERENCE: 00786/435003
16 <140> CURRENT APPLICATION NUMBER: 10/660,811
17 <141> CURRENT FILING DATE: 2003-09-12
19 <150> PRIOR APPLICATION NUMBER: US 60/410,376
20 <151> PRIOR FILING DATE: 2002-09-12
22 <150> PRIOR APPLICATION NUMBER: US 60/410,817
23 <151> PRIOR FILING DATE: 2002-09-13
25 <160> NUMBER OF SEQ ID NOS: 290
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

see pp 2-3

ERRORED SEQUENCES

```
8849 <210> SEQ ID NO: 234
8850 <211> LENGTH: 56
8851 <212> TYPE: PRT
8852 <213> ORGANISM: Pseudomonas aeruginosa
8854 <400> SEQUENCE: 234
```

see p. 2

E--> 8855
Gln Val Gln His Pro Cys Leu Leu Asp Gln His Gln Gln Glu Cys Ile Pro Pro Cys Leu Pro Pro Asp His

```
<210> 234
<211> 56
<212> PRT
<213> Pseudomonas aeruginosa

<400> 234
Gln Val Gln His Pro Cys Leu Leu Asp Gln His Gln Gln Glu Cys Ile Pro Pro Cys Leu
Pro Pro Asp His Leu Gln Asp Pro Gln His Pro Phe Leu Leu Pro Asp His His Val Pro
His Leu Val Val Leu Ile Gln Pro Gln Leu Cys Arg Ala Leu Ala Pro
```

insert a hard return

number the amino acids (see below)

hard return

1) Per 1.822 of Sequence Rules: a MAXIMUM of 16 amino acids per line

2) Number the amino acids under every 5 amino acids; do not use TAB codes between amino acid numbers. Use space characters.

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```
<210> 128
<211> 294
<212> PRT
<213> Pseudomonas aeruginosa

<220>
<221> misc_feature
<222> 711, 790, 795
<223> n = A,T,C or G

<400> 128
```

? *These apply to a nucleotide sequence only. Besides, only 294 amino acids are in Sequence 128.*

Please ensure the above error does not appear in subsequent sequences.

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

FYI. Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

```
L:3914 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:110
L:3918 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110 after pos.:180
M:341 Repeated in SeqNo=110
L:3944 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:111 after pos.:480
L:4037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:117 after pos.:360
L:4057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:118 after pos.:360
L:4198 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:122
L:4199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:122 after pos.:0
M:341 Repeated in SeqNo=122
L:4229 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:123
L:4230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123 after pos.:0
M:341 Repeated in SeqNo=123
L:4262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:124 after pos.:300
M:341 Repeated in SeqNo=124
L:4320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:126 after pos.:660
M:341 Repeated in SeqNo=126
L:8855 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:234
L:8855 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:8855 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:8855 M:252 E: No. of Seq. differs, <211> LENGTH:Input:56 Found:48 SEQ:234
L:8868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:235 after pos.:0
L:9420 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:263
L:9421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:263 after pos.:0
M:341 Repeated in SeqNo=263
L:9478 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265 after pos.:0
M:341 Repeated in SeqNo=265
```